This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-12. **(Cancelled)**

Claim 13. **(Currently amended)** A method for predicting phenotypic resistance of Human Deficiency Virus (HIV) to a therapeutic agent comprising:

(a) providing a neural network;

(b) training a neural network on a training data set, whereby the training data set is generated from a genotype-phenotype database, wherein each member of the training data set corresponds to a genetic mutation that correlates to a phenotypic resistance of HIV, said training being performed by

i) propagating a training data set in a feed-forward fashion,

ii) calculating the associated error,

iii) back propagating the error,

iv) adjusting the weights in the neural network,

v) minimizing the error function by repeating the steps i), ii), iii), iv),

vi) inputting a testing data set to ensure proper training, said testing data set comprising members that correspond to at least one genetic mutation, the presence of which correlates to a phenotypic resistance of HIV to at least one therapeutic agent, which testing data set is different from the training data set:

(c) providing a determined HIV genetic sequence from a patient by

i) obtaining an HIV sample from the patient,

ii) obtaining the genetic sequence from the HIV sample; and

d) predicting the phenotypic resistance of HIV to the therapeutic agent by inputting the determined genetic sequence into the trained neural network which computes the predicted phenotypic resistance of HIV to a therapeutic agent, wherein the phenotypic resistance is expressed as the fold-change in the IC_{50} or IC_{90} values of one or more therapeutic agents.

Claims 14-17. **(Cancelled)**

Claim 18. **(Original)** The method of claim 13, wherein the neural network is a three-layer feed-forward neural network.

Claim 19. **(Original)** The method of claim 18, wherein the three-layer feed forward network comprises:

(a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the pathogen;

(b) a plurality of hidden nodes; and

(c) a set of output nodes, wherein each member of the set of output nodes corresponds to a therapeutic agent used to treat the pathogen.

Claims 20-29. (Cancelled)